



SEQUENCE LISTING

<110> Payne, Jewel
Sick, August J.

<120> Novel *Bacillus thuringiensis* Isolate Active Against Lepidopteran Pests, and Genes Encoding Novel Lepidopteran-Active Toxins

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<151> 2000-03-09

<150> US 08/933,891
<151> 1997-09-19

<150> US 08/356,034
<151> 1994-12-14

<150> US 08/210,110
<151> 1994-03-17

<150> US 07/865,168
<151> 1992-04-09

<150> US 07/451,261
<151> 1989-12-14

<150> US 371,955
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<170> PatentIn version 3.2

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Pro Gly Ala Gly Phe Val Leu Gly Leu Ile Asp Leu Ile Trp Gly Phe
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Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu
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Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg
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Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu Ala Phe Arg
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Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Thr Glu Glu Met Arg
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Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu
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Phe Thr Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val Tyr Val Gln
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Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe Gly
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Gln Arg Trp Gly Phe Asp Val Ala Thr Ile Asn Ser Arg Tyr Asn Asp
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Arg Gln Pro His Leu Met Asp Leu Leu Asn Ser Ile Thr Ile Tyr Thr
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Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln Ile Thr Ala
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Ser Pro Val Gly Phe Ala Gly Pro Glu Phe Thr Phe Pro Arg Tyr Gly
325 330 335

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Gly Ser Gly Pro Asn Asn Gln Asn Leu Phe Val Leu Asp Gly Thr Glu
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Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro Gln Asp Asn
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Ser Val Pro Ala Arg Ala Gly Phe Ser His Arg Leu Ser His Val Thr
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Met Leu Ser Gln Ala Ala Gly Ala Val Tyr Thr Leu Arg Ala Pro Thr
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Phe Ser Trp Arg His Arg Ser Ala Glu Phe Ser Asn Leu Ile Pro Ser
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Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
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Val Tyr Ile Glu Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu
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Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Asn Arg
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Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
675 680 685

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690 695 700

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
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725 730 735

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu
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Asp Ser Gln His Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Thr Lys His
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Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Val
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Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Ile Gly Cys
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Met Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
850 855 860

Lys Pro Leu Val Gly Glu Ser Leu Ala Arg Val Lys Arg Ala Glu Lys
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Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Val Glu Thr Asn Ile Val
885 890 895

Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
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Tyr Asp Arg Leu Gln Ala Asp Thr Asp Ile Ala Met Ile His Ala Ala
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Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
930 935 940

Val Ile Pro Gly Val Asn Ala Gly Ile Phe Glu Glu Leu Glu Gly Arg
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Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
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Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val
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995 1000 1005

Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
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Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu
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Gly Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu
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Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn
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Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly
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Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Asn Leu Ile
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Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr
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Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile
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Thr Gly Leu Asp Asn Ser Asn Pro Val Ala Gly Ile Glu Gly Val Glu
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Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile
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Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala
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Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser
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Ala Ser Pro Thr Asn Glu Val Ser Pro Ser Arg Ile Thr Gln Ile Pro
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Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asp Val
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Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Ala Cys Leu Ser
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Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys
645 650 655

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
660 665 670

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
675 680 685

Asp Ile Thr Ile Gln Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
915 920 925

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
930 935 940

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
980 985 990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 995 1000 1005

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
 1010 1015 1020

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
 1025 1030 1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
 1040 1045 1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
 1055 1060 1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
 1070 1075 1080

Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr
 1085 1090 1095

Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu
 1100 1105 1110

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1115 1120 1125

Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp
 1130 1135 1140

Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val
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Glu Leu Leu Leu Met Glu Glu
 1160 1165

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 <211> 3567
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 <213> *Bacillus thuringiensis*

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gatTTTGTAT gggaaatagt tggcccttct caatggatg catttctagt acaaattgaa	240
caattaatta atgaaagaat agctgaattt gcttaggaatg ctgctattgc taatttagaa	300
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gctcaagcgg ccaatctgca tctagctata ttaagagattt ctgttaatttt tggagaaaga	540
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gtcacagcat ataaagaggg atatggagag ggctgcgtaa cgatccatgc gatcgaagac	3180
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gtacgtgtatcataattatac tggactcaa gaagaatatg agggtacgtt cacttctcg	3300
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ccagagaccg ataaggatg gattgagatc ggagaaacag aaggaacatt catcggttca	3540

agcgtggaat tactccttat ggaggaa 3567

<210> 6
<211> 1189
<212> PRT
<213> *Bacillus thuringiensis*

<400> 6

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Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
260 265 270

Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
275 280 285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
290 295 300

Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305 310 315 320

Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn
325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
340 345 350

Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
370 375 380

Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
385 390 395 400

Arg Gly Arg Gly Gln Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
435 440 445

Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
450 455 460

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
485 490 495

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
515 520 525

Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
530 535 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545 550 555 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
595 600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
645 650 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
675 680 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
690 695 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
725 730 735

Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
740 745 750

Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
755 760 765

Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
770 775 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
805 810 815

Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
835 840 845

Glu Asp Leu Gly Leu Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Asn
850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
915 920 925

Gln Val Asn Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
930 935 940

His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
965 970 975

Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
995 1000 1005

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala
1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1025 1030 1035

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val
1040 1045 1050

Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser
1055 1060 1065

Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
1070 1075 1080

Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr
 1085 1090 1095

Ser Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser
 1100 1105 1110

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr
 1115 1120 1125

Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly
 1130 1135 1140

Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu
 1145 1150 1155

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr
 1160 1165 1170

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu
 1175 1180 1185

Glu

<210> 7
 <211> 3522
 <212> DNA
 <213> *Bacillus thuringiensis*

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acacgttcc tttgagtga atttgttcca ggtgtggag ttgcgtttgg attatttgat	180
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gaatttagagt acttcccaga aaccgataag gtatggattg agatcggaga aacggaagga	3480
acattcatcg tggacagcgt ggaattactc cttatggagg aa	3522

<210> 8
 <211> 1174
 <212> PRT
 <213> **Bacillus thuringiensis**

<400> 8

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			20				25				30				

Pro Leu Asp Ile Ser Leu Ser Leu Thr Arg Phe Leu Leu Ser Glu Phe
 35 40 45

Val Pro Gly Val Gly Val Ala Phe Gly Leu Phe Asp Leu Ile Trp Gly
 50 55 60

Phe Ile Thr Pro Ser Asp Trp Ser Leu Phe Leu Leu Gln Ile Glu Gln
 65 70 75 80

Leu Ile Glu Gln Arg Ile Glu Thr Leu Glu Arg Asn Arg Ala Ile Thr
 85 90 95

Thr Leu Arg Gly Leu Ala Asp Ser Tyr Glu Ile Tyr Ile Glu Ala Leu
 100 105 110

Arg Glu Trp Glu Ala Asn Pro Asn Asn Ala Gln Leu Arg Glu Asp Val
 115 120 125

Arg Ile Arg Phe Ala Asn Thr Asp Asp Ala Leu Ile Thr Ala Ile Asn
 130 135 140

Asn Phe Thr Leu Thr Ser Phe Glu Ile Pro Leu Leu Ser Val Tyr Val
 145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Leu Leu Arg Asp Ala Val Ser Phe
 165 170 175

Gly Gln Gly Trp Gly Leu Asp Ile Ala Thr Val Asn Asn His Tyr Asn
 180 185 190

Arg Leu Ile Asn Leu Ile His Arg Tyr Thr Lys His Cys Leu Asp Thr
 195 200 205

Tyr Asn Gln Gly Leu Glu Asn Leu Arg Gly Thr Asn Thr Arg Gln Trp
 210 215 220

Ala Arg Phe Asn Gln Phe Arg Arg Asp Leu Thr Leu Thr Val Leu Asp
 225 230 235 240

Ile Val Ala Leu Phe Pro Asn Tyr Asp Val Arg Thr Tyr Pro Ile Gln
 245 250 255

Thr Ser Ser Gln Leu Thr Arg Glu Ile Tyr Thr Ser Ser Val Ile Glu
260 265 270

Asp Ser Pro Val Ser Ala Asn Ile Pro Asn Gly Phe Asn Arg Ala Glu
275 280 285

Phe Gly Val Arg Pro Pro His Leu Met Asp Phe Met Asn Ser Leu Phe
290 295 300

Val Thr Ala Glu Thr Val Arg Ser Gln Thr Val Trp Gly Gly His Leu
305 310 315 320

Val Ser Ser Arg Asn Thr Ala Gly Asn Arg Ile Asn Phe Pro Ser Tyr
325 330 335

Gly Val Phe Asn Pro Gly Gly Ala Ile Trp Ile Ala Asp Glu Asp Pro
340 345 350

Arg Pro Phe Tyr Arg Thr Leu Ser Asp Pro Val Phe Val Arg Gly Gly
355 360 365

Phe Gly Asn Pro His Tyr Val Leu Gly Leu Arg Gly Val Ala Phe Gln
370 375 380

Gln Thr Gly Thr Asn His Thr Arg Thr Phe Arg Asn Ser Gly Thr Ile
385 390 395 400

Asp Ser Leu Asp Glu Ile Pro Pro Gln Asp Asn Ser Gly Ala Pro Trp
405 410 415

Asn Asp Tyr Ser His Val Leu Asn His Val Thr Phe Val Arg Trp Pro
420 425 430

Gly Glu Ile Ser Gly Ser Asp Ser Trp Arg Ala Pro Met Phe Ser Trp
435 440 445

Thr His Arg Ser Ala Thr Pro Thr Asn Thr Ile Asp Pro Glu Arg Ile
450 455 460

Thr Gln Ile Pro Leu Val Lys Ala His Thr Leu Gln Ser Gly Thr Thr
465 470 475 480

Val Val Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr
485 490 495

Ser Gly Gly Pro Phe Ala Tyr Thr Ile Val Asn Ile Asn Gly Gln Leu
500 505 510

Pro Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu
515 520 525

Arg Ile Tyr Val Thr Val Ala Gly Glu Arg Ile Phe Ala Gly Gln Phe
530 535 540

Asn Lys Thr Met Asp Thr Gly Asp Pro Leu Thr Phe Gln Ser Phe Ser
545 550 555 560

Tyr Ala Thr Ile Asn Thr Ala Phe Thr Phe Pro Met Ser Gln Ser Ser
565 570 575

Phe Thr Val Gly Ala Asp Thr Phe Ser Ser Gly Asn Glu Val Tyr Ile
580 585 590

Asp Arg Phe Glu Leu Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr
595 600 605

Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ile
610 615 620

Asn Gln Ile Gly Ile Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
625 630 635 640

Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
645 650 655

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
660 665 670

Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Lys Gly Ile Asn Arg Gln
675 680 685

Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Arg Gly
690 695 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
705 710 715 720

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
725 730 735

Lys Pro Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln
740 745 750

Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
755 760 765

Asn Val Leu Gly Thr Gly Ser Leu Trp Pro Leu Ser Val Gln Ser Pro
770 775 780

Ile Arg Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
785 790 795 800

Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
805 810 815

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
820 825 830

Asn Glu Asp Leu Asp Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
835 840 845

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu
850 855 860

Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
865 870 875 880

Asp Lys Arg Glu Lys Leu Glu Leu Glu Thr Asn Ile Val Tyr Lys Glu
885 890 895

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Gln
900 905 910

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
915 920 925

Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
930 935 940

Gly Val Asn Val Asp Ile Phe Glu Glu Leu Lys Gly Arg Ile Phe Thr
945 950 955 960

Ala Phe Phe Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
965 970 975

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
980 985 990

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
995 1000 1005

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
1010 1015 1020

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val
1025 1030 1035

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
1040 1045 1050

Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
1055 1060 1065

Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr
1070 1075 1080

Ser Arg Asn Arg Gly Tyr Asp Glu Thr Tyr Gly Ser Asn Ser Ser
1085 1090 1095

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr
1100 1105 1110

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly
1115 1120 1125

Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu
1130 1135 1140

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr
1145 1150 1155

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu
1160 1165 1170

Glu

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<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> 42-mer oligonucleotide constructed to the sequence of the insert
in pM2,31-4

<400> 9
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<210> 10
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> 40-mer oligonucleotide constructed to the sequence of the insert
in pM2,31-1

<400> 10
gaagtttatg gccttttct gtagaaaatc aaattggacc 40